

-1-

## SEQUENCE LISTING

<110> Schrier, Peter I.  
 Aarnoudse, Corlien  
 Heider, Karl-Heinz  
 Klade, Christoph

<120> Camel, An Alternative Translation Product of the Tumor Antigen-Lage 1

<130> 0652.2200000

<140> 09/807,512  
 <141> 2001-04-16

<150> PCT/EP99/07832  
 <151> 1999-10-15

<150> EP 98119583.7  
 <151> 1998-10-16

<160> 28

<170> PatentIn Ver. 2.1

<210> 1  
 <211> 679  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 3'UTR  
 <222> (340)..(679)

<220>  
 <221> 5'UTR  
 <222> (1)..(9)

<220>  
 <221> CDS  
 <222> (10)..(339)

<400> 1

CGACGGGCG ATG CTG ATG GCC CAG GAG GCC CTG GCA TTC CTG ATG GCC	48
Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala	
1 5 10	

CAG GGG GCA ATG CTG GCG GCC CAG GAG AGG CGG GTG CCA CGG GCG GCA	96
Gln Gly Ala Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala	
15 20 25	

GAG GTC CCC GGG GCG CAG GGG CAA GGG CCT CGG GGC CGA GAG GAG	144
Glu Val Pro Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu	
30 35 40 45	

GCG CCC CGC GGG GTC CGC ATG GCG GTG CCG CTT CTG CGC AGG ATG GAA	192
Ala Pro Arg Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu	

-2-

50                          55                          60

GGT GCC CCT GCG GGG CCA GGA GGC CGG ACA GCC GCC TGC TTC AGT TGC Gly Ala Pro Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys	65 70 75	240
ACA TCA CGA TGC CTT TCT CGT CGC CCA TGG AAG CGG AGC TGG TCC GCA Thr Ser Arg Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala	80 85 90	288
GGA TCC TGT CCC GGG ATG CCG CAC CTC TCC CCC GAC CAG GGG CGG TTC Gly Ser Cys Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe	95 100 105	336
TGA AGGACTTCAC CGTGTCCGGC AACCTACTGT TTATCCGACT GACTGCTGCA		389
GACCACCGCC AACTGCAGCT CTCCATCAGC TCCTGTCTCC AGCAGCTTTC CCTGTTGATG		449
TGGATCACGC AGTGCTTTCT GCCCGTGTTC TTGGCTCAGG CTCCCTCAGG GCAGAGGCCGC		509
TAAGCCCCAGC CTGGCGCCCC TTCCTAGGTC ATGCCTCCTC CCCTAGGGAA TGGTCCCAGC		569
ACGAGTGGCC AGTTCATTTGT GGGGGCCTGA TTGTTGTGCG CTGGAGGAGG ACGGCTTACA		629
TGTTTGTTC TGTAGAAAAT AAAGCTGAGC TACGAAAAAA AAAAAAAAAA		679

<210> 2  
<211> 109  
<212> PRT  
<213> Homo sapiens

<400> 2

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala  
1 5 10 15

Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro  
20 25 30

Gly Ala Gln Gly Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
35 40 45

Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro  
50 55 60

Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg  
65 70 75 80

Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys  
85 90 95

Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe  
          , 100                  105

<210> 3

-3-

<211> 767  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> CDS  
<222> (54)..(596)

<220>  
<221> 3' UTR  
<222> (597)..(767)

<220>  
<221> 5'UTR  
<222> (1)..(53)

<400> 3

-4-

ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG GCT CCC TCA GGG Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly 165 170 175	584
CAG AGG CGC TAA GCCCAGCCTG GCGCCCCCTTC CTAGGTCAATG CCTCCTCCCC Gln Arg Arg 180	636
TAGGGAATGG TCCCAGCACG AGTGGCCAGT TCATTGTGGG GGCCTGATTG TTTGTCGCTG GAGGAGGACG GCTTACATGT TTGTTCTGT AGAAAATAAA GCTGAGCTAC GAAAAAAA AAAAAAAAA A	696
	756
	767

<210> 4  
<211> 180  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp 1 5 10 15
Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly 20 25 30
Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala 35 40 45
Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro 50 55 60
His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala 65 70 75 80
Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe 85 90 95
Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp 100 105 110
Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val 115 120 125
Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln 130 135 140
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met 145 150 155 160
Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser 165 170 175
Gly Gln Arg Arg 180

<210> 5  
<211> 993  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> 5'UTR  
<222> (1)..(55)

<220>  
<221> CDS  
<222> (56) .. (688)

<220>  
<221> 3' UTR  
<222> (689) .. (993)

<400> 5

GCATCCTCGT	GGGCCCTGAC	CTTCTCTCTG	AGAGCCGGGC	AGAGGCTCCG	GAGCC	ATG										
						Met										
						1										
CAG	GCC	GAA	GGC	CAG	GGC	ACA	GGG	GGT	TCG	ACG	GGC	GAT	GCT	GAT	GGC	
Gln	Ala	Glu	Gly	Gln	Gly	Thr	Gly	Gly	Ser	Thr	Gly	Asp	Ala	Asp	Gly	
				5					10					15		
CCA	GGA	GGC	CCT	GGC	ATT	CCT	GAT	GGC	CCA	GGG	GGC	AAT	GCT	GGC	GGC	
Pro	Gly	Gly	Pro	Gly	Ile	Pro	Asp	Gly	Pro	Gly	Gly	Asn	Ala	Gly	Gly	
				20					25					30		
CCA	GGA	GAG	GCG	GGT	GCC	ACG	GGC	GGC	AGA	GGT	CCC	CGG	GGC	GCA	GGG	
Pro	Gly	Glu	Ala	Gly	Ala	Thr	Gly	Gly	Arg	Gly	Pro	Arg	Gly	Ala	Gly	
				35					40					45		
GCA	GCA	AGG	GCC	TCG	GGG	CCG	AGA	GGA	GGC	GCC	CCG	CGG	GGT	CCG	CAT	
Ala	Ala	Arg	Ala	Ser	Gly	Pro	Arg	Gly	Gly	Ala	Pro	Arg	Gly	Pro	His	
				50					55					60		
GGC	GGT	GCC	GCT	TCT	CGC	CAG	GAT	GGA	AGG	TGC	CCC	TGC	GGG	GCC	AGG	
Gly	Gly	Ala	Ala	Ser	Ala	Gln	Asp	Gly	Arg	Cys	Pro	Cys	Gly	Ala	Arg	
				70					75					80		
AGG	CCG	GAC	AGC	CGC	CTG	CTT	CAG	TTG	CAC	ATC	ACG	ATG	CCT	TTC	TCG	
Arg	Pro	Asp	Ser	Arg	Leu	Leu	Gln	Leu	His	Ile	Thr	Met	Pro	Phe	Ser	
				85					90					95		
TCG	CCC	ATG	GAA	GCG	GAG	CTG	GTC	CGC	AGG	ATC	CTG	TCC	CGG	GAT	GCC	
Ser	Pro	Met	Glu	Ala	Glu	Leu	Val	Arg	Arg	Ile	Leu	Ser	Arg	Asp	Ala	
				100					105					110		
GCA	CCT	CTC	CCC	CGA	CCA	GGG	GCG	GTT	CTG	AAG	GAC	TTC	ACC	GTG	TCC	
Ala	Pro	Leu	Pro	Arg	Pro	Gly	Ala	Val	Leu	Lys	Asp	Phe	Thr	Val	Ser	
				115					120					125		
GGC	AAC	CTA	CTG	TTT	ATG	TCA	GTT	CGG	GAC	CAG	GAC	AGG	GAA	GGC	GCT	
Gly	Asn	Leu	Leu	Phe	Met	Ser	Val	Arg	Asp	Gln	Asp	Arg	Glu	Gly	Ala	
				130					135					140		
GGG	CGG	ATG	AGG	GTG	GTG	GGT	TGG	GGG	CTG	GGA	TCC	GCC	TCC	CCG	GAG	
Gly	Arg	Met	Arg	Val	Val	Gly	Trp	Gly	Leu	Gly	Ser	Ala	Ser	Pro	Glu	
				150					155					160		

-6-

GGG CAG AAA GCT AGA GAT CTC AGA ACA CCC AAA CAC AAG GTC TCA GAA Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser Glu 165 170 175	586
CAG AGA CCT GGT ACA CCA GGC CCG CCG CCA CCC GAG GGA GCC CAG GGA Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Glu Gly Ala Gln Gly 180 185 190	634
GAT GGG TGC AGA GGT GTC GCC TTT AAT GTG ATG TTC TCT GCC CCT CAC Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro His 195 200 205	682
ATT TAG CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC ATCAGCTCCT Ile 210	738
GTCTCCAGCA GCTTCCCTG TTGATGTGGA TCACGCAGTG CTTTCTGCC GTGTTTTGG 798	
CTCAGGCTCC CTCAGGGCAG AGGCGCTAACG CCCAGCCTGG CGCCCCTTCC TAGGTCATGC 858	
CTCCTCCCCT AGGGAATGGT CCCAGCACGA GTGGCCAGTT CATTGTGGGG GCCTGATTGT 918	
TTGTCGCTGG AGGAGGACGG CTTACATGTT TGTTCTGTA GAAAATAAAG CTGAGCTACG 978	
AAAAAAAAAA AAAAAA 993	
<210> 6	
<211> 210	
<212> PRT	
<213> Homo sapiens	
<400> 6	
Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp 1 5 10 15	
Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly 20 25 30	
Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala 35 40 45	
Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro 50 55 60	
His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala 65 70 75 80	
Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe 85 90 95	
Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp 100 105 110	
Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val 115 120 125	
Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly 130 135 140	
Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro 145 150 155 160	

-7-

Glu	Gly	Gln	Lys	Ala	Arg	Asp	Leu	Arg	Thr	Pro	Lys	His	Lys	Val	Ser
				165					170					175	
Glu	Gln	Arg	Pro	Gly	Thr	Pro	Gly	Pro	Pro	Pro	Glu	Gly	Ala	Gln	
				180				185				190			
Gly	Asp	Gly	Cys	Arg	Gly	Val	Ala	Phe	Asn	Val	Met	Phe	Ser	Ala	Pro
				195			200				205				
His	Ile														
	210														

<210> 7  
<211> 752  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> (1)..(53)

<220>  
<221> CDS  
<222> (54)..(596)

<220>  
<221> 3'UTR  
<222> (597)..(752)

<400> 7

ATCCTCGTGG	GCCCTGACCT	TCTCTCTGAG	AGCCGGGCAG	AGGCTCCGGA	GCC	ATG	56									
						Met										
						1										
CAG	GCC	GAA	GGC	CGG	GGC	ACA	GGG	GGT	TCG	ACG	GGC	GAT	GCT	GAT	GGC	104
Gln	Ala	Glu	Gly	Arg	Gly	Thr	Gly	Gly	Ser	Thr	Gly	Asp	Ala	Asp	Gly	
				5				10					15			
CCA	GGA	GGC	CCT	GGC	ATT	CCT	GAT	GGC	CCA	GGG	GGC	AAT	GCT	GGC	GGC	152
Pro	Gly	Gly	Pro	Gly	Ile	Pro	Asp	Gly	Pro	Gly	Gly	Asn	Ala	Gly	Gly	
				20			25					30				
CCA	GGA	GAG	GCG	GGT	GCC	ACG	GGC	GGC	AGA	GGT	CCC	CGG	GGC	GCA	GGG	200
Pro	Gly	Glu	Ala	Ala	Thr	Gly	Gly	Arg	Gly	Pro	Arg	Gly	Ala	Gly		
				35			40				45					
GCA	GCA	AGG	GCC	TCG	GGG	CCG	GGA	GGA	GGC	GCC	CCG	CGG	GGT	CCG	CAT	248
Ala	Ala	Arg	Ala	Ser	Gly	Pro	Gly	Gly	Gly	Ala	Pro	Arg	Gly	Pro	His	
				50			55			60			65			
GGC	GGC	GCG	GCT	TCA	GGG	CTG	AAT	GGA	TGC	TGC	AGA	TGC	GGG	GCC	AGG	296
Gly	Gly	Ala	Ala	Ser	Gly	Leu	Asn	Gly	Cys	Cys	Arg	Cys	Gly	Ala	Arg	
				70				75					80			
GGG	CCG	GAG	AGC	CGC	CTG	CTT	GAG	TTC	TAC	CTC	GCC	ATG	CCT	TTC	GCG	344
Gly	Pro	Glu	Ser	Arg	Leu	Leu	Glu	Phe	Tyr	Leu	Ala	Met	Pro	Phe	Ala	

-8-

	85	90	95	
ACA CCC ATG GAA GCA GAG CTG GCC CGC AGG AGC CTG GCC CAG GAT GCC Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala	100	105	110	392
CCA CCG CTT CCC GTG CCA GGG GTG CTT CTG AAG GAG TTC ACT GTG TCC Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser	115	120	125	440
GGC AAC ATA CTG ACT ATC CGA CTG ACT GCT GCA GAC CAC CGC CAA CTG Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu	130	135	140	488
CAG CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp	150	155	160	536
ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly	165	170	175	584
CAG AGG CGC TAA GCCCAGCCTG GCGCCCCCTTC CTAGGTCAATG CCTCCTCCCC Gln Arg Arg	180			636
TAGGGAATGG TCCCAGCACG AGTGGCCAGT TCATTGTGGG GGCCTGATTG TTTGTCGCTG				696
GAGGGAGGACG GCTTACATGT TTGTTCTGT AGAAAAATAAA ACTGAGCTAC GAAAAAA				752

<210> 8  
<211> 180  
<212> PRT  
<213> Homo sapiens

<400> 8

Met	Gln	Ala	Glu	Gly	Arg	Gly	Thr	Gly	Gly	Ser	Thr	Gly	Asp	Ala	Asp
1															15
Gly	Pro	Gly	Gly	Pro	Gly	Ile	Pro	Asp	Gly	Pro	Gly	Gly	Asn	Ala	Gly
															30
Gly	Pro	Gly	Glu	Ala	Gly	Ala	Thr	Gly	Gly	Arg	Gly	Pro	Arg	Gly	Ala
															45
Gly	Ala	Ala	Arg	Ala	Ser	Gly	Pro	Gly	Gly	Ala	Pro	Arg	Gly	Pro	
															60
His	Gly	Gly	Ala	Ala	Ser	Gly	Leu	Asn	Gly	Cys	Cys	Arg	Cys	Gly	Ala
															80
Arg	Gly	Pro	Glu	Ser	Arg	Leu	Leu	Glu	Phe	Tyr	Leu	Ala	Met	Pro	Phe
															95
Ala	Thr	Pro	Met	Glu	Ala	Glu	Leu	Ala	Arg	Arg	Ser	Leu	Ala	Gln	Asp
															110
Ala	Pro	Pro	Leu	Pro	Val	Pro	Gly	Val	Leu	Leu	Lys	Glu	Phe	Thr	Val
															125

-9-

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln  
 130 135 140

Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met  
 145 150 155 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser  
 165 170 175

Gly Gln Arg Arg  
 180

<210> 9  
 <211> 752  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> (1)..(93)

<220>  
 <221> CDS  
 <222> (94)..(270)

<220>  
 <221> 3'UTR  
 <222> (271)..(752)

<400> 9

ATCCTCGTGG GCCCTGACCT TCTCTTGAG AGCCGGGCAG AGGCTCCGGA GCCATGCAGG 60

CCGAAGGCCG GGGCACAGGG GGTCGACGG GCG ATG CTG ATG GCC CAG GAG GCC 114  
 Met Leu Met Ala Gln Glu Ala  
 1 5

CTG GCA TTC CTG ATG GCC CAG GGG GCA ATG CTG GCG GCC CAG GAG AGG 162  
 Leu Ala Phe Leu Met Ala Gln Gly Ala Met Leu Ala Ala Gln Glu Arg  
 10 15 20

CGG GTG CCA CGG GCG GCA GAG GTC CCC GGG GCG CAG GGG CAG CAA GGG 210  
 Arg Val Pro Arg Ala Ala Glu Val Pro Gly Ala Gln Gly Gln Gln Gly  
 25 30 35

CCT CGG GGC CGG GAG GAG GCG CCC CGC GGG GTC CGC ATG GCG GCG CGG 258  
 Pro Arg Gly Arg Glu Ala Pro Arg Gly Val Arg Met Ala Ala Arg  
 40 45 50 55

CTT CAG GGC TGA ATGGATGCTG CAGATGCGGG GCCAGGGGG CGGAGAGCCG 310  
 Leu Gln Gly

CCTGCTTGAG TTCTACCTCG CCATGCCTTT CGCGACACCC ATGGAAGCAG AGCTGGCCCG 370

CAGGAGCCTG GCCCAGGATG CCCCACCGCT TCCCGTGCCA GGGGTGCTTC TGAAGGAGTT 430

CACTGTGTCC GGCAACATAC TGACTATCCG ACTGACTGCT GCAGACCACC GCCAACTGCA 490

GCTCTCCATC AGCTCCTGTC TCCAGCAGCT TTCCCTGTTG ATGTGGATCA CGCAGTGCTT 550

-10-

TCTGCCCGTG TTTTGGCTC AGCCTCCCTC AGGGCAGAGG CGCTAAGCCC AGCCTGGCGC 610  
CCCTTCCTAG GTCATGCCTC CTCCCCTAGG GAATGGTCCC AGCACGAGTG GCCAGTTCAT 670  
TGTGGGGGCC TGATTGTTG TCGCTGGAGG AGGACGGCTT ACATGTTGT TTCTGTAGAA 730  
AATAAAAATG AGCTACGAAA AA 752

<210> 10  
<211> 58  
<212> PRT  
<213> Homo sapiens

<400> 10

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala  
1 5 10 15  
Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro  
20 25 30  
Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
35 40 45  
Gly Val Arg Met Ala Ala Arg Leu Gln Gly  
50 55

<210> 11  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 11

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu  
1 5 10

<210> 12  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 12

Leu Met Ala Gln Glu Ala Leu Ala Phe Leu  
1 5 10

<210> 13  
<211> 21  
<212> DNA  
<213> Artificial Sequence

-11-

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

GGTGACACTA TAGAAGGTAC G

21

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

TGATGTGCAA CTGAAGCAGG

20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

GCAC TGC GTG ATCC ACATCA A

21

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

CGACTCACTA TAGGGAGAGA G

21

<210> 17

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

GCACATCACG ATGCCTTCT CGTCG

25

-12-

<210> 18  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 18

CACACAAAGC TTGGCTTAGC GCCTCTGCC TG

32

<210> 19  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 19

CACACAGGAT CCATGGATGC TGCAGATGCG

30

<210> 20  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 20

GAAGAACATA TGCTGATGGC CCAGGAGGC

29

<210> 21  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 21

TTAAAGATCT CAGAACCGCC CCTGGTCG

28

<210> 22  
<211> 25  
<212> DNA  
<213> Artificial Sequence

09807512

-13-

<220>  
<223> Description of Artificial Sequence: Primer

<400> 22

TTACTCGAGA TGCTGATGGC CCAGG

25

<210> 23  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 23

AAGGTACCTT GAACCGCCCC TGGTCG

26

<210> 24  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 24

Phe Leu Met Ala Gln Gly Ala Met Leu  
1 5

<210> 25  
<211> 10  
<212> PRT  
<213> Homo sapiens

<400> 25

Ala Met Leu Ala Ala Gln Glu Arg Arg Val  
1 5 10

<210> 26  
<211> 9  
<212> PRT  
<213> Homo sapiens

<400> 26

Met Leu Ala Ala Gln Glu Arg Arg Val  
1 5

<210> 27  
<211> 10  
<212> PRT  
<213> Homo sapiens

09807512 09807512  
09807512

-14-

<400> 27

Tyr Tyr Met Asn Gly Thr Met Ser Gln Val  
1 5 10

<210> 28

<211> 9

<212> PRT

<213> Homo sapiens

<400> 28

Glu Val Asp Pro Ile Gly His Leu Tyr  
1 5